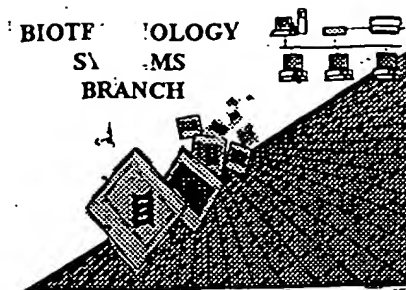


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/744,489

Source: PC109

Date Processed by STIC: 10/30/01

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/744,489

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- Numbering
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- "bug"
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                              (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                              This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    (NEW RULES)            <210> sequence id number  
                              <400> sequence id number  
                              000
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                              In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
    Response                scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                              is Artificial Sequence
- 11 ✓ Use of <220>            Sequence(s)   4   missing the <220> "Feature" and associated numeric identifiers and responses.  
                              Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                              "Unknown." Please explain source of genetic material in <220> to <223> section.  
                              (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
    "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                              listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,489

DATE: 10/30/2001

TIME: 13:15:14

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\10302001\I744489.raw

**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Drewe, Lisa  
 4 Brightwell, Gale  
 5 Howlett, Elizabeth  
 7 <120> TITLE OF INVENTION: Nucleic Acid Detection Method by Triple Helix Formation  
 9 <130> FILE REFERENCE: 41577-252464  
 11 <140> CURRENT APPLICATION NUMBER: US 09/744,489  
 12 <141> CURRENT FILING DATE: 2001-01-23  
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/02317  
 15 <151> PRIOR FILING DATE: 1999-07-19  
 17 <160> NUMBER OF SEQ ID NOS: 4  
 19 <170> SOFTWARE: PatentIn version 3.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 82  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <223> OTHER INFORMATION: PCR product  
 29 <400> SEQUENCE: 1  
 30 ataaatacaa ccaacaaaat aaatagtcac aaaattgtat acattagcaa tgcataccac 60  
 32 aaagttctaa gtactaaaat at 82  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 185  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Artificial Sequence  
 40 <220> FEATURE:  
 41 <223> OTHER INFORMATION: PCR product  
 43 <400> SEQUENCE: 2  
 44 gcgaaacgga acatagccca aaccaagagg cttgcctctt ggggttgtag gacattctat 60  
 46 acggagttac aaaggaagca ggtagacgaa gcgacctgga aaggccgctc gtagagggta 120  
 48 acaaccccggt agtcgaaact tcgttctctc ttgaatgtat cctgagtacg gcggaacacg 180  
 50 tgaac 185  
 53 <210> SEQ ID NO: 3  
 54 <211> LENGTH: 15  
 55 <212> TYPE: DNA  
 56 <213> ORGANISM: Artificial Sequence  
 58 <220> FEATURE:  
 59 <223> OTHER INFORMATION: Peptide nucleic acid probe  
 61 <400> SEQUENCE: 3  
 62 ttttccttcc ctttt 15  
 65 <210> SEQ ID NO: 4  
 66 <211> LENGTH: 33  
 67 <212> TYPE: DNA  
 68 <213> ORGANISM: Artificial Sequence  
 70 <220> FEATURE:  
 71 <223> OTHER INFORMATION: Peptide nucleic acid  
 73 <220> FEATURE:  
 74 <221> NAME/KEY: misc\_feature

(mixture of amino + nucleic acid?)  
 7 → unacceptable explanation  
 See error summary sheet, Item 11

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,489

DATE: 10/30/2001

TIME: 13:15:14

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\10302001\I744489.raw

75 &lt;222&gt; LOCATION: (16)..(16)

76 <223> OTHER INFORMATION: n represents a Lysine residue hydrophilic linker

79 &lt;220&gt; FEATURE:

80 &lt;221&gt; NAME/KEY: misc\_feature

81 &lt;222&gt; LOCATION: (17)..(17)

82 <223> OTHER INFORMATION: n represents a Lysine residue hydrophilic linker

85 &lt;220&gt; FEATURE:

86 &lt;221&gt; NAME/KEY: misc\_feature

87 &lt;222&gt; LOCATION: (18)..(18)

88 <223> OTHER INFORMATION: n represents a Lysine residue hydrophilic linker

91 &lt;400&gt; SEQUENCE: 4

W--&gt; 92 ttttcccttc cttttnnntt ttccttcctt ttt

33

*"n" can only represent a nucleic acid; an amino acid cannot be used*

*same*

*same*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/744,489

DATE: 10/30/2001

TIME: 13:15:15

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\10302001\I744489.raw

L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4